



## SEQUENCE LISTING

<110> MOULAND, Andrew S.  
COHEN, Eric A.  
WICKHAM, Louise  
LUO, Ming  
DUCHAIINE, Thomas

<120> MAMMALIAN STAUFEN AND USE THEREOF

<130> 10875-77

<140> 09/316,048

<141> 1999-05-21

<150> CA 2,238,656

<151> 1998-05-22

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 3142

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (3)..(1775)

<400> 1

ac ttc ctg ccg ggc tgc ggg cgc ctg agc gct ctt cag cgt ttg cgc 47  
Phe Leu Pro Gly Cys Gly Arg Leu Ser Ala Leu Gln Arg Leu Arg

1 5 10 15

ggc ggc tgc gcg tct ctc tcg gct ccc gct tcc ttt gac cgc ctc ccc 95  
Gly Gly Cys Ala Ser Leu Ser Ala Pro Ala Ser Phe Asp Arg Leu Pro

20 25 30

ccc ccg gcc cgg cgg cgc ccg cct cct cca cgg cca ctc cgc ctc ttc 143  
Pro Pro Ala Arg Arg Arg Pro Pro Pro Pro Arg Pro Leu Arg Leu Phe

35 40 45

cct ccc ttc gtc cct tct tcc tct ccc ttt ttt cct tct tcc ttc ccc 191  
Pro Pro Phe Val Pro Ser Ser Ser Pro Phe Phe Pro Ser Ser Phe Pro

50 55 60

tcc tcg ccg cca ccg ccc agg acc gcc ggc cgg ggg acg agc tcg gag 239  
Ser Ser Pro Pro Pro Pro Arg Thr Ala Gly Arg Gly Thr Ser Ser Glu

65 70 75

cag cag cca gaa agc ata acc cct act gta gaa cta aat gca ctg tgc 287  
Gln Gln Pro Glu Ser Ile Thr Pro Thr Val Glu Leu Asn Ala Leu Cys

80	85	90	95	
atg aaa ctt gga aaa aaa cca atg tat aag cct gtt gac cct tac tct				335
Met Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr Ser	100	105	110	
cgg atg cag tcc acc tat aac tac aac atg aga gga ggt gct tat ccc				383
Arg Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr Pro	115	120	125	
cgg agg tac ttt tac cca ttt cca gtt cca cct tta ctt tat caa gtg				431
Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln Val	130	135	140	
gaa ctt tct gtg gga gga cag caa ttt aat ggc aaa gga aag aca aga				479
Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr Arg	145	150	155	
cag gct gcg aaa cac gat gct gct gcc aaa gcg ttg agg atc ctg cag				527
Gln Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu Gln	160	165	170	175
aat gag ccc ctg cca gag agg ctg gag gtg aat gga aga gaa tcc gaa				575
Asn Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser Glu	180	185	190	
gaa gaa aat ctc aat aaa tct gaa ata agt caa gtg ttt gag att gca				623
Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile Ala	195	200	205	
ctt aaa cgg aac ttg cct gtg aat ttc gag gtg gcc cgg gag agt ggc				671
Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser Gly	210	215	220	
cca ccc cac atg aag aac ttt gtg acc aag gtt tgc gtt ggg gag ttt				719
Pro Pro His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu Phe	225	230	235	
gtg ggg gaa ggt gaa ggg aaa agc aag aag att tca aag aaa aat gcc				767
Val Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn Ala	240	245	250	255
gcc ata gct gtt ctt gag gag ctg aag aag tta ccg ccc ctg cct gca				815
Ala Ile Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro Ala	260	265	270	
gtt gaa cga gta aag cct aga atc aaa aag aaa aca aaa ccc ata gtc				863
Val Glu Arg Val Lys Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile Val	275	280	285	
aag cca cag aca agc cca gaa tat ggc cag ggg atc aat ccg att agc				911
Lys Pro Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile Ser	290	295	300	

cga ctg gcc cag atc cag cag gca aaa aag gag aag gag cca gag tac	959
Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu Tyr	
305 310 315	
acg ctc ctc aca gag cga ggc ctc ccg cgc cgc agg gag ttt gtg atg	1007
Thr Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe Val Met	
320 325 330 335	
cag gtg aag gtt gga aac cac act gca gaa gga acg ggc acc aac aag	1055
Gln Val Lys Val Gly Asn His Thr Ala Glu Gly Thr Gly Thr Asn Lys	
340 345 350	
aag gtg gcc aag cgc aat gca gcc gag aac atg ctg gag atc ctt ggt	1103
Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu Gly	
355 360 365	
ttc aaa gtc ccg cag cgg cag ccc acc aaa ccc gca ctc aag tca gag	1151
Phe Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser Glu	
370 375 380	
gag aag aca ccc ata aag aaa cca ggg gat gga aga aaa gta acc ttt	1199
Glu Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr Phe	
385 390 395	
ttt gaa cct ggc tct ggg gat gaa aat ggg act agt aat aaa gag gat	1247
Phe Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu Asp	
400 405 410 415	
gag ttc agg atg cct tat cta agt cat cag cag ctg cct gct gga att	1295
Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly Ile	
420 425 430	
ctt ccc atg gtg ccc gag gtc gcc cag gct gta gga gtt agt caa gga	1343
Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln Gly	
435 440 445	
cat cac acc aaa gat ttt acc agg gca gct ccg aat cct gcc aag gcc	1391
His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys Ala	
450 455 460	
acg gta act gcc atg ata gcc cga gag ttg ttg tat ggg ggc acc tcg	1439
Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr Ser	
465 470 475	
ccc aca gcc gag acc att tta aag aat aac atc tct tca ggc cac gta	1487
Pro Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser Ser Gly His Val	
480 485 490 495	
ccc cat gga cct ctc acg aga ccc tct gag caa ctg gac tat ctt tcc	1535
Pro His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu Ser	
500 505 510	
aga gtc cag gga ttc cag gtt gaa tac aaa gac ttc ccc aaa aac aac	1583
Arg Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn Asn	

515	520	525	
aag aac gaa ttt gta tct ctt atc aat tgc tcc tct cag cca cct ctg			1631
Lys Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro Leu			
530	535	540	
atc agc cat ggt atc ggc aag gat gtg gag tcc tgc cat gat atg gct			1679
Ile Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met Ala			
545	550	555	
gcg ctg aac atc tta aag ttg ctg tct gag ttg gac caa caa agt aca			1727
Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser Thr			
560	565	570	575
gag atg cca aga aca gga aac gga cca atg tct gtg tgt ggg agg tgc			1775
Glu Met Pro Arg Thr Gly Asn Gly Pro Met Ser Val Cys Gly Arg Cys			
580	585	590	
tgaacctttt ctggccatga accattataa aatcccaaca tatatactga aaatactgaa			1835
actgctttga aaatttgga tttctgatac ctccagtggg ccgagagaca cgggtgggtaa			1895
aggatgtggg cagcagcagg gaagacaaca gaaacacaag gaggcggctg tggccggctg			1955
gactgtgctg gggtttggtg tgatggccac tcgggtgacct ggcggtcctt acgcaatagc			2015
agctgcctgt ggggaagaag ggctgcccag ccagctgggt ctcccgggac accagcagat			2075
ccacaccctg ggcacctccg tgtttgggtct tttttttccc ctgtgtgaaa gaagaaacgg			2135
cacgaccctt tctcaagctg gtcactcag acacattggg acaaaccctg gacagccatg			2195
ccagagagag gcctttgacc ggccccagag ctaaaagcac cagagaaaat caaatgcttc			2255
ctactcagcg tgacccaact tttctagtgt gccacggccc caccacctcc tgcagtaccc			2315
acaccatcac cactgcttcc tttccaaca gtgatctgta ttcttagttt cattattttc			2375
ttttgattga tatgacacta tataaaattt tcatttgaga atttctcaat tgtatctagt			2435
taaatagcac agtttggaag cttgtctgag actgacttta tcaataatct aaccgacaaa			2495
gatcatatcc atgtgtatgt ggtagacat ttttatttca ttgactaacc caggacagtt			2555
tcagtgatgc aaattgtgtg ccctctggtt cagctgaaac agtctgggac tttcaaaaac			2615
cttgaataag tctccacag ttgtataaat tggacaattt aggaatttta aacttttagat			2675
gatcatttgg ttccattttt atttcatttt tatttttggtt aatgcaaaca ggacttaa			2735
gaactttgat ctctgtttta aagattatta aaaaacattg tgtatctata catatggctc			2795
ttgaggactt agctttcact acactacagg atatgatctc catgtagtcc atataaacct			2855

gcagagtgat tttccagagt gctcgatact gttaattaca tctccattag ggctgaaaag 2915  
aatgacctac gtttctgtat acagctgtgt tgcttttgat gttgtgttac tgtacacaga 2975  
agtgtgtgca ctgaggctct gcgtgtggtc cgtatggaaa acctggtagc cctgcgagtt 3035  
aagtactgct tccattcatt gtttacgctg gaatttttct ccccatggaa tgtaagtaaa 3095  
acttaagtgt ttgtcatcaa taaatggtaa tactaaaaaa aaaaaaa 3142

<210> 2  
<211> 591  
<212> PRT  
<213> Homo sapiens

<400> 2  
Phe Leu Pro Gly Cys Gly Arg Leu Ser Ala Leu Gln Arg Leu Arg Gly  
1 5 10 15  
Gly Cys Ala Ser Leu Ser Ala Pro Ala Ser Phe Asp Arg Leu Pro Pro  
20 25 30  
Pro Ala Arg Arg Arg Pro Pro Pro Pro Arg Pro Leu Arg Leu Phe Pro  
35 40 45  
Pro Phe Val Pro Ser Ser Ser Pro Phe Phe Pro Ser Ser Phe Pro Ser  
50 55 60  
Ser Pro Pro Pro Pro Arg Thr Ala Gly Arg Gly Thr Ser Ser Glu Gln  
65 70 75 80  
Gln Pro Glu Ser Ile Thr Pro Thr Val Glu Leu Asn Ala Leu Cys Met  
85 90 95  
Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr Ser Arg  
100 105 110  
Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr Pro Pro  
115 120 125  
Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln Val Glu  
130 135 140  
Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr Arg Gln  
145 150 155 160  
Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu Gln Asn  
165 170 175  
Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser Glu Glu  
180 185 190  
Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile Ala Leu

195						200						205					
Lys	Arg	Asn	Leu	Pro	Val	Asn	Phe	Glu	Val	Ala	Arg	Glu	Ser	Gly	Pro		
210						215						220					
Pro	His	Met	Lys	Asn	Phe	Val	Thr	Lys	Val	Ser	Val	Gly	Glu	Phe	Val		
225			230						235			240					
Gly	Glu	Gly	Glu	Gly	Lys	Ser	Lys	Lys	Ile	Ser	Lys	Lys	Asn	Ala	Ala		
			245						250			255					
Ile	Ala	Val	Leu	Glu	Glu	Leu	Lys	Lys	Leu	Pro	Pro	Leu	Pro	Ala	Val		
			260						265			270					
Glu	Arg	Val	Lys	Pro	Arg	Ile	Lys	Lys	Lys	Thr	Lys	Pro	Ile	Val	Lys		
275						280						285					
Pro	Gln	Thr	Ser	Pro	Glu	Tyr	Gly	Gln	Gly	Ile	Asn	Pro	Ile	Ser	Arg		
290						295						300					
Leu	Ala	Gln	Ile	Gln	Gln	Ala	Lys	Lys	Glu	Lys	Glu	Pro	Glu	Tyr	Thr		
305			310						315			320					
Leu	Leu	Thr	Glu	Arg	Gly	Leu	Pro	Arg	Arg	Arg	Glu	Phe	Val	Met	Gln		
			325						330			335					
Val	Lys	Val	Gly	Asn	His	Thr	Ala	Glu	Gly	Thr	Gly	Thr	Asn	Lys	Lys		
			340						345			350					
Val	Ala	Lys	Arg	Asn	Ala	Ala	Glu	Asn	Met	Leu	Glu	Ile	Leu	Gly	Phe		
355						360						365					
Lys	Val	Pro	Gln	Arg	Gln	Pro	Thr	Lys	Pro	Ala	Leu	Lys	Ser	Glu	Glu		
370			375						380								
Lys	Thr	Pro	Ile	Lys	Lys	Pro	Gly	Asp	Gly	Arg	Lys	Val	Thr	Phe	Phe		
385			390						395			400					
Glu	Pro	Gly	Ser	Gly	Asp	Glu	Asn	Gly	Thr	Ser	Asn	Lys	Glu	Asp	Glu		
			405						410			415					
Phe	Arg	Met	Pro	Tyr	Leu	Ser	His	Gln	Gln	Leu	Pro	Ala	Gly	Ile	Leu		
420						425						430					
Pro	Met	Val	Pro	Glu	Val	Ala	Gln	Ala	Val	Gly	Val	Ser	Gln	Gly	His		
435						440						445					
His	Thr	Lys	Asp	Phe	Thr	Arg	Ala	Ala	Pro	Asn	Pro	Ala	Lys	Ala	Thr		
450			455						460								
Val	Thr	Ala	Met	Ile	Ala	Arg	Glu	Leu	Leu	Tyr	Gly	Gly	Thr	Ser	Pro		
465			470						475			480					
Thr	Ala	Glu	Thr	Ile	Leu	Lys	Asn	Asn	Ile	Ser	Ser	Gly	His	Val	Pro		

	485		490		495
His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu Ser Arg					
	500		505		510
Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn Asn Lys					
	515		520		525
Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro Leu Ile					
	530		535		540
Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met Ala Ala					
545		550		555	560
Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser Thr Glu					
	565		570		575
Met Pro Arg Thr Gly Asn Gly Pro Met Ser Val Cys Gly Arg Cys					
	580		585		590

<210> 3  
 <211> 3217  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (363)..(1850)

<400> 3  
 acttctgccc gggctgcggg cgctgagcg ctcttcagcg ttgcgcggc ggctgcgcgt 60  
 ctctctcggc tcccgttcc ttgaccgcc tcccccccc ggcccggcgg cgcccgcctc 120  
 ctccacgggc actccgcctc ttccctccct tegtcccttc ttctctccc ttttttctt 180  
 ctctctccc ctctcgccg ccaccgccca ggaccgccgg ccgggggacg agctcggagc 240  
 agcagccaga gtttattaac cacttaacct ctcagaactg acaaagaca acattgttcc 300  
 tggaacgccc tcttttttaa aaagaaagca taaccctac tgtagaacta aatgcactgt 360  
 gc atg aaa ctt gga aaa aaa cca atg tat aag cct gtt gac cct tac 407  
 Met Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr  
 1 5 10 15  
 tct cgg atg cag tcc acc tat aac tac aac atg aga gga ggt gct tat 455  
 Ser Arg Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr  
 20 25 30  
 ccc ccg agg tac ttt tac cca ttt cca gtt cca cct tta ctt tat caa 503  
 Pro Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln

	35	40	45	
gtg gaa ctt tct gtg gga gga cag caa ttt aat ggc aaa gga aag aca	551			
Val Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr				
50 55 60				
aga cag gct gcg aaa cac gat gct gct gcc aaa gcg ttg agg atc ctg	599			
Arg Gln Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu				
65 70 75				
cag aat gag ccc ctg cca gag agg ctg gag gtg aat gga aga gaa tcc	647			
Gln Asn Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser				
80 85 90 95				
gaa gaa gaa aat ctc aat aaa tct gaa ata agt caa gtg ttt gag att	695			
Glu Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile				
100 105 110				
gca ctt aaa cgg aac ttg cct gtg aat ttc gag gtg gcc cgg gag agt	743			
Ala Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser				
115 120 125				
ggc cca ccc cac atg aag aac ttt gtg acc aag gtt tcg gtt ggg gag	791			
Gly Pro Pro His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu				
130 135 140				
ttt gtg ggg gaa ggt gaa ggg aaa agc aag aag att tca aag aaa aat	839			
Phe Val Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn				
145 150 155				
gcc gcc ata gct gtt ctt gag gag ctg aag aag tta ccg ccc ctg cct	887			
Ala Ala Ile Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro				
160 165 170 175				
gca gtt gaa cga gta aag cct aga atc aaa aag aaa aca aaa ccc ata	935			
Ala Val Glu Arg Val Lys Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile				
180 185 190				
gtc aag cca cag aca agc cca gaa tat ggc cag ggg atc aat ccg att	983			
Val Lys Pro Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile				
195 200 205				
agc cga ctg gcc cag atc cag cag gca aaa aag gag aag gag cca gag	1031			
Ser Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu				
210 215 220				
tac acg ctc ctc aca gag cga ggc ctc ccg cgc cgc agg gag ttt gtg	1079			
Tyr Thr Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe Val				
225 230 235				
atg cag gtg aag gtt gga aac cac act gca gaa gga acg ggc acc aac	1127			
Met Gln Val Lys Val Gly Asn His Thr Ala Glu Gly Thr Gly Thr Asn				
240 245 250 255				



aag aag gtg gcc aag cgc aat gca gcc gag aac atg ctg gag atc ctt	1175
Lys Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu	
260 265 270	
ggt ttc aaa gtc ccg cag cgg cag ccc acc aaa ccc gca ctc aag tca	1223
Gly Phe Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser	
275 280 285	
gag gag aag aca ccc ata aag aaa cca ggg gat gga aga aaa gta acc	1271
Glu Glu Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr	
290 295 300	
ttt ttt gaa cct ggc tct ggg gat gaa aat ggg act agt aat aaa gag	1319
Phe Phe Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu	
305 310 315	
gat gag ttc agg atg cct tat cta agt cat cag cag ctg cct gct gga	1367
Asp Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly	
320 325 330 335	
att ctt ccc atg gtg ccc gag gtc gcc cag gct gta gga gtt agt caa	1415
Ile Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln	
340 345 350	
gga cat cac acc aaa gat ttt acc agg gca gct ccg aat cct gcc aag	1463
Gly His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys	
355 360 365	
gcc acg gta act gcc atg ata gcc cga gag ttg ttg tat ggg ggc acc	1511
Ala Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr	
370 375 380	
tcg ccc aca gcc gag acc att tta aag aat aac atc tct tca ggc cac	1559
Ser Pro Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser Ser Gly His	
385 390 395	
gta ccc cat gga cct ctc acg aga ccc tct gag caa ctg gac tat ctt	1607
Val Pro His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu	
400 405 410 415	
tcc aga gtc cag gga ttc cag gtt gaa tac aaa gac ttc ccc aaa aac	1655
Ser Arg Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn	
420 425 430	
aac aag aac gaa ttt gta tct ctt atc aat tgc tcc tct cag cca cct	1703
Asn Lys Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro	
435 440 445	
ctg atc agc cat ggt atc ggc aag gat gtg gag tcc tgc cat gat atg	1751
Leu Ile Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met	
450 455 460	
gct gcg ctg aac atc tta aag ttg ctg tct gag ttg gac caa caa agt	1799
Ala Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser	

465

470

475

aca gag atg cca aga aca gga aac gga cca atg tct gtg tgt ggg agg 1847  
 Thr Glu Met Pro Arg Thr Gly Asn Gly Pro Met Ser Val Cys Gly Arg  
 480 485 490 495

tgc tgaacctttt ctggccatga accattataa aatcccaaca tatatactga 1900  
 Cys

aaatactgaa actgctttga aaatttggaa tttctgatac ctccagtggg ccgagagaca 1960

cgggtgggtaa aggatgtggg cagcagcagg gaagacaaca gaaacacaag gaggcggctg 2020

tggccggctg gactgtgctg gggtttgttg tgatggccac tcggtgacct ggcggtccct 2080

acgcaatagc agctgcctgt ggggaagaag ggctgccag ccagctgggt ctcccgggac 2140

accagcagat ccacaccctg ggcacctccg tgtttggtct ttttttccc ctgtgtgaaa 2200

gaagaaacgg cagacccct tctcaagctg gctcactcag acacattggg acaaaccctg 2260

gacagccatg ccagagagag gcctttgacc ggccccagag ctaaaagcac cagagaaaat 2320

caaatgcttc ctactcagcg tgaccaact tttctagtgt gccacggccc caccacctcc 2380

tgcagtacc acaccatcac cactgcttcc tttccaaca gtgatctgta ttcttagttt 2440

cattattttc ttttgattga tatgacacta tataaaattt tcatttgaga atttctcaat 2500

tgtatctagt taaatagcac agtttggaaa cttgtctgag actgacttta tcaataatct 2560

aaccgacaaa gatcatatcc atgtgtatgt ggtagacat tttatttca ttgactaacc 2620

caggacagtt tcagtgatgc aaattgtgtg cctctgggt cagctgaaac agtctggac 2680

tttcaaaaac cttgaataag tctcccacag ttgtataaat tggacaattt aggaatttta 2740

aactttagat gatcatttgg ttccattttt atttcatttt tatttttgtt aatgcaaaca 2800

ggacttaa at gaactttgat ctctgtttta aagattatta aaaaacattg tgtatctata 2860

catatggctc ttgaggactt agctttcact acactacagg atatgatctc catgtagtcc 2920

atataaacct gcagagtgat tttccagagt gctcgatact gttaattaca tctccattag 2980

ggctgaaaag aatgacctac gtttctgtat acagctgtgt tgcttttgat gttgtgttac 3040

tgtacacaga agtgtgtgca ctgaggctct gcgtgtggtc cgtatggaaa acctggtagc 3100

cctgcgagtt aagtactgct tccattcatt gtttacgctg gaatttttct ccccatggaa 3160

tgtaagtaaa acttaagtgt ttgtcatcaa taaatggtaa tactaaaaaa aaaaaa 3217

<210> 4  
<211> 496  
<212> PRT  
<213> Homo sapiens

<400> 4

Met	Lys	Leu	Gly	Lys	Lys	Pro	Met	Tyr	Lys	Pro	Val	Asp	Pro	Tyr	Ser	
1				5				10						15		
Arg	Met	Gln	Ser	Thr	Tyr	Asn	Tyr	Asn	Met	Arg	Gly	Gly	Ala	Tyr	Pro	
			20					25						30		
Pro	Arg	Tyr	Phe	Tyr	Pro	Phe	Pro	Val	Pro	Pro	Leu	Leu	Tyr	Gln	Val	
			35				40					45				
Glu	Leu	Ser	Val	Gly	Gly	Gln	Gln	Phe	Asn	Gly	Lys	Gly	Lys	Thr	Arg	
	50					55					60					
Gln	Ala	Ala	Lys	His	Asp	Ala	Ala	Ala	Lys	Ala	Leu	Arg	Ile	Leu	Gln	
65					70					75					80	
Asn	Glu	Pro	Leu	Pro	Glu	Arg	Leu	Glu	Val	Asn	Gly	Arg	Glu	Ser	Glu	
				85					90					95		
Glu	Glu	Asn	Leu	Asn	Lys	Ser	Glu	Ile	Ser	Gln	Val	Phe	Glu	Ile	Ala	
			100					105					110			
Leu	Lys	Arg	Asn	Leu	Pro	Val	Asn	Phe	Glu	Val	Ala	Arg	Glu	Ser	Gly	
		115					120					125				
Pro	Pro	His	Met	Lys	Asn	Phe	Val	Thr	Lys	Val	Ser	Val	Gly	Glu	Phe	
	130					135						140				
Val	Gly	Glu	Gly	Glu	Gly	Lys	Ser	Lys	Lys	Ile	Ser	Lys	Lys	Asn	Ala	
145					150					155					160	
Ala	Ile	Ala	Val	Leu	Glu	Glu	Leu	Lys	Lys	Leu	Pro	Pro	Leu	Pro	Ala	
				165					170						175	
Val	Glu	Arg	Val	Lys	Pro	Arg	Ile	Lys	Lys	Lys	Thr	Lys	Pro	Ile	Val	
			180					185					190			
Lys	Pro	Gln	Thr	Ser	Pro	Glu	Tyr	Gly	Gln	Gly	Ile	Asn	Pro	Ile	Ser	
		195					200					205				
Arg	Leu	Ala	Gln	Ile	Gln	Gln	Ala	Lys	Lys	Glu	Lys	Glu	Pro	Glu	Tyr	
	210					215					220					
Thr	Leu	Leu	Thr	Glu	Arg	Gly	Leu	Pro	Arg	Arg	Arg	Glu	Phe	Val	Met	
225					230					235					240	
Gln	Val	Lys	Val	Gly	Asn	His	Thr	Ala	Glu	Gly	Thr	Gly	Thr	Asn	Lys	
				245					250						255	

Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu Gly  
 260 265 270  
 Phe Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser Glu  
 275 280 285  
 Glu Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr Phe  
 290 295 300  
 Phe Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu Asp  
 305 310 315 320  
 Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly Ile  
 325 330 335  
 Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln Gly  
 340 345 350  
 His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys Ala  
 355 360 365  
 Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr Ser  
 370 375 380  
 Pro Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser Ser Gly His Val  
 385 390 395 400  
 Pro His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu Ser  
 405 410 415  
 Arg Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn Asn  
 420 425 430  
 Lys Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro Leu  
 435 440 445  
 Ile Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met Ala  
 450 455 460  
 Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser Thr  
 465 470 475 480  
 Glu Met Pro Arg Thr Gly Asn Gly Pro Met Ser Val Cys Gly Arg Cys  
 485 490 495

<210> 5  
 <211> 3506  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> (409) .. (2139)

<400> 5

```
acttcctgcc gggctgcggg cgctgagcg ctcttcagcg tttgcgcggc ggctgcgcgt 60
ctctctcggc tcccgttcc tttgaccgcc tccccccccc ggcccggcgg cgccgcctc 120
ctccaaggcc actcgcctc ttccctccct tcgtcccttc ttcctctccc ttttttcctt 180
cttccttccc ctctcgccg ccaccgcca ggaccgcgg ccgggggacg agctcggagc 240
agcagccaga gtttattaac cacttaacct ctcagaactg aacaagaca acattgttcc 300
tggaacgccc tctttttaaa aaaggtagaa ctttagactt catagcactg aattaacctg 360
cactgaaagc tgtttacctg catttgttca cttttgttga aagtgacc atg tct caa 417
                                     Met Ser Gln
                                     1
gtt caa gtg caa gtt cag aac cca tct gct gct ctc tca ggg agc caa 465
Val Gln Val Gln Val Gln Asn Pro Ser Ala Ala Leu Ser Gly Ser Gln
      5              10              15
ata ctg aac aag aac cag tct ctt ctc tca cag cct ttg atg agt att 513
Ile Leu Asn Lys Asn Gln Ser Leu Leu Ser Gln Pro Leu Met Ser Ile
      20              25              30              35
cct tct act act agc tct ctg ccc tct gaa aat gca ggt aga ccc att 561
Pro Ser Thr Thr Ser Ser Leu Pro Ser Glu Asn Ala Gly Arg Pro Ile
              40              45              50
caa aac tct gct tta ccc tct gca tct att aca tcc acc agt gca gct 609
Gln Asn Ser Ala Leu Pro Ser Ala Ser Ile Thr Ser Thr Ser Ala Ala
              55              60              65
gca gaa agc ata acc cct act gta gaa cta aat gca ctg tgc atg aaa 657
Ala Glu Ser Ile Thr Pro Thr Val Glu Leu Asn Ala Leu Cys Met Lys
              70              75              80
ctt gga aaa aaa cca atg tat aag cct gtt gac cct tac tct cgg atg 705
Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr Ser Arg Met
              85              90              95
cag tcc acc tat aac tac aac atg aga gga ggt gct tat ccc ccg agg 753
Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr Pro Pro Arg
100              105              110              115
tac ttt tac cca ttt cca gtt cca cct tta ott tat caa gtg gaa ctt 801
Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln Val Glu Leu
              120              125              130
tct gtg gga gga cag caa ttt aat ggc aaa gga aag aca aga cag gct 849
Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr Arg Gln Ala
              135              140              145
```

gcg aaa cac gat gct gct gcc aaa gcg ttg agg atc ctg cag aat gag	897
Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu Gln Asn Glu	
150 155 160	
ccc ctg cca gag agg ctg gag gtg aat gga aga gaa tcc gaa gaa gaa	945
Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser Glu Glu Glu	
165 170 175	
aat ctc aat aaa tct gaa ata agt caa gtg ttt gag att gca ctt aaa	993
Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile Ala Leu Lys	
180 185 190 195	
cgg aac ttg cct gtg aat ttc gag gtg gcc cgg gag agt ggc cca ccc	1041
Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser Gly Pro Pro	
200 205 210	
cac atg aag aac ttt gtg acc aag gtt tcg gtt ggg gag ttt gtg ggg	1089
His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu Phe Val Gly	
215 220 225	
gaa ggt gaa ggg aaa agc aag aag att tca aag aaa aat gcc gcc ata	1137
Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn Ala Ala Ile	
230 235 240	
gct gtt ctt gag gag ctg aag aag tta ccg ccc ctg cct gca gtt gaa	1185
Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro Ala Val Glu	
245 250 255	
cga gta aag cct aga atc aaa aag aaa aca aaa ccc ata gtc aag cca	1233
Arg Val Lys Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile Val Lys Pro	
260 265 270 275	
cag aca agc cca gaa tat ggc cag ggg atc aat ccg att agc cga ctg	1281
Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile Ser Arg Leu	
280 285 290	
gcc cag atc cag cag gca aaa aag gag aag gag cca gag tac acg ctc	1329
Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu Tyr Thr Leu	
295 300 305	
ctc aca gag cga ggc ctc ccg cgc cgc agg gag ttt gtg atg cag gtg	1377
Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe Val Met Gln Val	
310 315 320	
aag gtt gga aac cac act gca gaa gga acg ggc acc aac aag aag gtg	1425
Lys Val Gly Asn His Thr Ala Glu Gly Thr Gly Thr Asn Lys Lys Val	
325 330 335	
gcc aag cgc aat gca gcc gag aac atg ctg gag atc ctt ggt ttc aaa	1473
Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu Gly Phe Lys	
340 345 350 355	
gtc ccg cag cgg cag ccc acc aaa ccc gca ctc aag tca gag gag aag	1521
Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser Glu Glu Lys	

360										365					370					
aca	ccc	ata	aag	aaa	cca	ggg	gat	gga	aga	aaa	gta	acc	ttt	ttt	gaa	1569				
Thr	Pro	Ile	Lys	Lys	Pro	Gly	Asp	Gly	Arg	Lys	Val	Thr	Phe	Phe	Glu					
			375					380					385							
cct	ggc	tct	ggg	gat	gaa	aat	ggg	act	agt	aat	aaa	gag	gat	gag	ttc	1617				
Pro	Gly	Ser	Gly	Asp	Glu	Asn	Gly	Thr	Ser	Asn	Lys	Glu	Asp	Glu	Phe					
		390					395					400								
agg	atg	cct	tat	cta	agt	cat	cag	cag	ctg	cct	gct	gga	att	ctt	ccc	1665				
Arg	Met	Pro	Tyr	Leu	Ser	His	Gln	Gln	Leu	Pro	Ala	Gly	Ile	Leu	Pro					
	405					410					415									
atg	gtg	ccc	gag	gtc	gcc	cag	gct	gta	gga	gtt	agt	caa	gga	cat	cac	1713				
Met	Val	Pro	Glu	Val	Ala	Gln	Ala	Val	Gly	Val	Ser	Gln	Gly	His	His					
420					425				430						435					
acc	aaa	gat	ttt	acc	agg	gca	gct	ccg	aat	cct	gcc	aag	gcc	acg	gta	1761				
Thr	Lys	Asp	Phe	Thr	Arg	Ala	Ala	Pro	Asn	Pro	Ala	Lys	Ala	Thr	Val					
			440					445						450						
act	gcc	atg	ata	gcc	cga	gag	ttg	ttg	tat	ggg	ggc	acc	tcg	ccc	aca	1809				
Thr	Ala	Met	Ile	Ala	Arg	Glu	Leu	Leu	Tyr	Gly	Gly	Thr	Ser	Pro	Thr					
			455				460						465							
gcc	gag	acc	att	tta	aag	aat	aac	atc	tct	tca	ggc	cac	gta	ccc	cat	1857				
Ala	Glu	Thr	Ile	Leu	Lys	Asn	Asn	Ile	Ser	Ser	Gly	His	Val	Pro	His					
		470					475					480								
gga	cct	ctc	acg	aga	ccc	tct	gag	caa	ctg	gac	tat	ctt	tcc	aga	gtc	1905				
Gly	Pro	Leu	Thr	Arg	Pro	Ser	Glu	Gln	Leu	Asp	Tyr	Leu	Ser	Arg	Val					
	485					490					495									
cag	gga	ttc	cag	gtt	gaa	tac	aaa	gac	ttc	ccc	aaa	aac	aac	aag	aac	1953				
Gln	Gly	Phe	Gln	Val	Glu	Tyr	Lys	Asp	Phe	Pro	Lys	Asn	Asn	Lys	Asn					
500				505					510					515						
gaa	ttt	gta	tct	ctt	atc	aat	tgc	tcc	tct	cag	cca	cct	ctg	atc	agc	2001				
Glu	Phe	Val	Ser	Leu	Ile	Asn	Cys	Ser	Ser	Gln	Pro	Pro	Leu	Ile	Ser					
				520				525						530						
cat	ggt	atc	ggc	aag	gat	gtg	gag	tcc	tgc	cat	gat	atg	gct	gcg	ctg	2049				
His	Gly	Ile	Gly	Lys	Asp	Val	Glu	Ser	Cys	His	Asp	Met	Ala	Ala	Leu					
			535				540						545							
aac	atc	tta	aag	ttg	ctg	tct	gag	ttg	gac	caa	caa	agt	aca	gag	atg	2097				
Asn	Ile	Leu	Lys	Leu	Leu	Ser	Glu	Leu	Asp	Gln	Gln	Ser	Thr	Glu	Met					
		550					555					560								
cca	aga	aca	gga	aac	gga	cca	atg	tct	gtg	tgt	ggg	agg	tgc			2139				
Pro	Arg	Thr	Gly	Asn	Gly	Pro	Met	Ser	Val	Cys	Gly	Arg	Cys							
	565					570					575									

tgaacctttt ctggccatga accattataa aatcccaaca tatatactga aaatactgaa 2199  
 actgctttga aaatttggaa tttctgatac ctccagtggg ccgagagaca cgggtgggtaa 2259  
 aggatgtggg cagcagcagg gaagacaaca gaaacacaag gaggcggctg tggccggctg 2319  
 gactgtgctg gggtttgttg tgatggccac tcggtgacct ggcggtccct acgcaatagc 2379  
 agctgcctgt ggggaagaag ggctgcccag ccagctgggt ctcccgggac accagcagat 2439  
 ccacaccctg ggcacctcgg tgtttgggtct tttttttccc ctgtgtgaaa gaagaaacgg 2499  
 cacgaccctt tctcaagctg gctcactcag acacattggg acaaaccctg gacagccatg 2559  
 ccagagagag gcctttgacc ggccccagag ctaaaagcac cagagaaaat caaatgcttc 2619  
 ctactcagcg tgaccaact tttctagtgt gccacggccc caccacctcc tgcagtaccc 2679  
 acaccatcac cactgctttc tttccaaca gtgatctgta ttcttagttt cattattttc 2739  
 ttttgattga tatgacacta tataaaatct tcatttgaga atttctcaat tgtatctagt 2799  
 taaatagcac agtttggaaa cttgtctgag actgacttta tcaataatct aaccgacaaa 2859  
 gatcatatcc atgtgtatgt ggtagacat ttttatttca ttgactaacc caggacagtt 2919  
 tcagtgatgc aaattgtgtg cctctctggt cagctgaaac agtcctggac tttcaaaaac 2979  
 cttgaataag tctccacag ttgtataaat tggacaattt aggaatttta aacttttagat 3039  
 gatcatttgg ttccattttt atttcatttt tatttttgtt aatgcaaaca ggacttaaat 3099  
 gaactttgat ctctgtttta aagattatta aaaaacattg tgtatctata catatggctc 3159  
 ttgaggactt agctttcact acactacagg atatgatctc catgtagtcc atataaacct 3219  
 gcagagtgat tttccagagt gctcgatact gttaattaca tctccattag ggctgaaaag 3279  
 aatgacctac gtttctgtat acagctgtgt tgcttttgat gttgtgttac tgtacacaga 3339  
 agtgtgtgca ctgaggctct gcgtgtggtc cgtatggaaa acctggtagc cctgcgagtt 3399  
 aagtactgct tccattcatt gtttacgctg gaatttttct ccccatggaa tgtaagtaaa 3459  
 acttaagtgt ttgtcatcaa taaatggtaa tactaaaaaa aaaaaaa 3506

<210> 6

<211> 577

<212> PRT

<213> Homo sapiens

<400> 6

Met Ser Gln Val Gln Val Gln Val Gln Asn Pro Ser Ala Ala Leu Ser



1	5	10	15
Gly Ser Gln Ile Leu Asn Lys Asn Gln Ser Leu Leu Ser Gln Pro Leu	20	25	30
Met Ser Ile Pro Ser Thr Thr Ser Ser Leu Pro Ser Glu Asn Ala Gly	35	40	45
Arg Pro Ile Gln Asn Ser Ala Leu Pro Ser Ala Ser Ile Thr Ser Thr	50	55	60
Ser Ala Ala Ala Glu Ser Ile Thr Pro Thr Val Glu Leu Asn Ala Leu	65	70	75
Cys Met Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr	85	90	95
Ser Arg Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr	100	105	110
Pro Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln	115	120	125
Val Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr	130	135	140
Arg Gln Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu	145	150	155
Gln Asn Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser	165	170	175
Glu Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile	180	185	190
Ala Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser	195	200	205
Gly Pro Pro His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu	210	215	220
Phe Val Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn	225	230	235
Ala Ala Ile Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro	245	250	255
Ala Val Glu Arg Val Lys Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile	260	265	270
Val Lys Pro Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile	275	280	285
Ser Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu			

290					295					300					
Tyr	Thr	Leu	Leu	Thr	Glu	Arg	Gly	Leu	Pro	Arg	Arg	Arg	Glu	Phe	Val
305					310					315					320
Met	Gln	Val	Lys	Val	Gly	Asn	His	Thr	Ala	Glu	Gly	Thr	Gly	Thr	Asn
				325					330					335	
Lys	Lys	Val	Ala	Lys	Arg	Asn	Ala	Ala	Glu	Asn	Met	Leu	Glu	Ile	Leu
			340					345					350		
Gly	Phe	Lys	Val	Pro	Gln	Arg	Gln	Pro	Thr	Lys	Pro	Ala	Leu	Lys	Ser
		355					360					365			
Glu	Glu	Lys	Thr	Pro	Ile	Lys	Lys	Pro	Gly	Asp	Gly	Arg	Lys	Val	Thr
	370					375					380				
Phe	Phe	Glu	Pro	Gly	Ser	Gly	Asp	Glu	Asn	Gly	Thr	Ser	Asn	Lys	Glu
385						390					395				400
Asp	Glu	Phe	Arg	Met	Pro	Tyr	Leu	Ser	His	Gln	Gln	Leu	Pro	Ala	Gly
				405					410					415	
Ile	Leu	Pro	Met	Val	Pro	Glu	Val	Ala	Gln	Ala	Val	Gly	Val	Ser	Gln
			420					425					430		
Gly	His	His	Thr	Lys	Asp	Phe	Thr	Arg	Ala	Ala	Pro	Asn	Pro	Ala	Lys
		435					440					445			
Ala	Thr	Val	Thr	Ala	Met	Ile	Ala	Arg	Glu	Leu	Leu	Tyr	Gly	Gly	Thr
				450			455					460			
Ser	Pro	Thr	Ala	Glu	Thr	Ile	Leu	Lys	Asn	Asn	Ile	Ser	Ser	Gly	His
465						470					475				480
Val	Pro	His	Gly	Pro	Leu	Thr	Arg	Pro	Ser	Glu	Gln	Leu	Asp	Tyr	Leu
				485				490						495	
Ser	Arg	Val	Gln	Gly	Phe	Gln	Val	Glu	Tyr	Lys	Asp	Phe	Pro	Lys	Asn
			500					505					510		
Asn	Lys	Asn	Glu	Phe	Val	Ser	Leu	Ile	Asn	Cys	Ser	Ser	Gln	Pro	Pro
			515				520					525			
Leu	Ile	Ser	His	Gly	Ile	Gly	Lys	Asp	Val	Glu	Ser	Cys	His	Asp	Met
	530					535					540				
Ala	Ala	Leu	Asn	Ile	Leu	Lys	Leu	Leu	Ser	Glu	Leu	Asp	Gln	Gln	Ser
545						550					555				560
Thr	Glu	Met	Pro	Arg	Thr	Gly	Asn	Gly	Pro	Met	Ser	Val	Cys	Gly	Arg
				565					570					575	

Cys

<210> 7  
<211> 3348  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (494) .. (1981)

<400> 7  
acttcctgcc gggctgcggg cgctgagcg ctcttcagcg ttgogcggc ggctgcgcgt 60  
  
ctctctcggc tcccgcttcc ttgaccgcc tcccccccc ggcccgggcg cgcccgctc 120  
  
ctccacggcc actccgcctc ttccctccct tegtcccttc ttcctctccc ttttttccct 180  
  
cttccttccc ctctcgccg ccaccgcca ggaccgcgg ccgggggacg agtcgggagc 240  
  
agcagccagc agcagccagg tggagttttg ctcttgctgc ccaggctgga gtgcagtggc 300  
  
gtgatctcgg ctcaactgcaa cctccacctc ccaggtcagc gattttccca cttcagcctc 360  
  
ccgataagct gagattacag agtttattaa ccacttaacc tctcagaact gaacaaagac 420  
  
aacattgttc ctggaacgcc ctcttttttaaaaagaaagc ataacccta ctgtagaact 480  
  
aatgcactg tgc atg aaa ctt gga aaa aaa cca atg tat aag cct gtt 529  
Met Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val  
1 5 10  
  
gac cct tac tct cgg atg cag tcc acc tat aac tac aac atg aga gga 577  
Asp Pro Tyr Ser Arg Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly  
15 20 25  
  
ggc gct tat ccc ccg agg tac ttt tac cca ttt cca gtt cca cct tta 625  
Gly Ala Tyr Pro Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu  
30 35 40  
  
ctt tat caa gtg gaa ctt tct gtg gga gga cag caa ttt aat ggc aaa 673  
Leu Tyr Gln Val Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys  
45 50 55 60  
  
gga aag aca aga cag gct gcg aaa cac gat gct gct gcc aaa gcg ttg 721  
Gly Lys Thr Arg Gln Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu  
65 70 75  
  
agg atc ctg cag aat gag ccc ctg cca gag agg ctg gag gtg aat gga 769  
Arg Ile Leu Gln Asn Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly  
80 85 90

aga gaa tcc gaa gaa gaa aat ctc aat aaa tct gaa ata agt caa gtg	817
Arg Glu Ser Glu Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val	
95 100 105	
ttt gag att gca ctt aaa cgg aac ttg cct gtg aat ttc gag gtg gcc	865
Phe Glu Ile Ala Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala	
110 115 120	
cgg gag agt ggc cca ccc cac atg aag aac ttt gtg acc aag gtt tcg	913
Arg Glu Ser Gly Pro Pro His Met Lys Asn Phe Val Thr Lys Val Ser	
125 130 135 140	
gtt ggg gag ttt gtg ggg gaa ggt gaa ggg aaa agc aag aag att tca	961
Val Gly Glu Phe Val Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser	
145 150 155	
aag aaa aat gcc gcc ata gct gtt ctt gag gag ctg aag aag tta ccg	1009
Lys Lys Asn Ala Ala Ile Ala Val Leu Glu Glu Leu Lys Lys Leu Pro	
160 165 170	
ccc ctg cct gca gtt gaa cga gta aag cct aga atc aaa aag aaa aca	1057
Pro Leu Pro Ala Val Glu Arg Val Lys Pro Arg Ile Lys Lys Lys Thr	
175 180 185	
aaa ccc ata gtc aag cca cag aca agc cca gaa tat ggc cag ggg atc	1105
Lys Pro Ile Val Lys Pro Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile	
190 195 200	
aat ccg att agc cga ctg gcc cag atc cag cag gca aaa aag gag aag	1153
Asn Pro Ile Ser Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys	
205 210 215 220	
gag cca gag tac acg ctc ctc aca gag cga ggc ctc ccg cgc cgc agg	1201
Glu Pro Glu Tyr Thr Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg	
225 230 235	
gag ttt gtg atg cag gtg aag gtt gga aac cac act gca gaa gga acg	1249
Glu Phe Val Met Gln Val Lys Val Gly Asn His Thr Ala Glu Gly Thr	
240 245 250	
ggc acc aac aag aag gtg gcc aag cgc aat gca gcc gag aac atg ctg	1297
Gly Thr Asn Lys Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu	
255 260 265	
gag atc ctt ggt ttc aaa gtc ccg cag cgg cag ccc acc aaa ccc gca	1345
Glu Ile Leu Gly Phe Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala	
270 275 280	
ctc aag tca gag gag aag aca ccc ata aag aaa cca ggg gat gga aga	1393
Leu Lys Ser Glu Glu Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg	
285 290 295 300	
aaa gta acc ttt ttt gaa cct ggc tct ggg gat gaa aat ggg act agt	1441
Lys Val Thr Phe Phe Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser	

305	310	315	
aat aaa gag gat gag ttc agg atg cct tat cta agt cat cag cag ctg			1489
Asn Lys Glu Asp Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu			
320	325	330	
cct gct gga att ctt ccc atg gtg ccc gag gtc gcc cag gct gta gga			1537
Pro Ala Gly Ile Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly			
335	340	345	
gtt agt caa gga cat cac acc aaa gat ttt acc agg gca gct ccg aat			1585
Val Ser Gln Gly His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn			
350	355	360	
cct gcc aag gcc acg gta act gcc atg ata gcc cga gag ttg ttg tat			1633
Pro Ala Lys Ala Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr			
365	370	375	380
ggg ggc acc tcg ccc aca gcc gag acc att tta aag aat aac atc tct			1681
Gly Gly Thr Ser Pro Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser			
385	390	395	
tca ggc cac gta ccc cat gga cct ctg acg aga ccc tct gag caa ctg			1729
Ser Gly His Val Pro His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu			
400	405	410	
gac tat ctt tcc aga gtc cag gga ttc cag gtt gaa tac aaa gac ttc			1777
Asp Tyr Leu Ser Arg Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe			
415	420	425	
ccc aaa aac aac aag aac gaa ttt gta tct ctt atc aat tgc tcc tct			1825
Pro Lys Asn Asn Lys Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser			
430	435	440	
cag cca cct ctg atc agc cat ggt atc ggc aag gat gtg gag tcc tgc			1873
Gln Pro Pro Leu Ile Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys			
445	450	455	460
cat gat atg gct gcg ctg aac atc tta aag ttg ctg tct gag ttg gac			1921
His Asp Met Ala Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp			
465	470	475	
caa caa agt aca gag atg cca aga aca gga aac gga cca atg tct gtg			1969
Gln Gln Ser Thr Glu Met Pro Arg Thr Gly Asn Gly Pro Met Ser Val			
480	485	490	
tgt ggg agg tgc tgaacctttt ctggccatga accattataa aatcccaaca			2021
Cys Gly Arg Cys			
495			
tatatactga aaatactgaa actgctttga aaatttgga tttctgatac ctccagtggg			2081
cogagagaca cggtgggtaa aggatgtggg cagcagcagg gaagacaaca gaaacacaag			2141

gaggcggctg tggccggctg gactgtgctg gggtttggtg tgatggccac tcggtgacct 2201  
ggcggtccct acgcaatagc agctgcctgt ggggaagaag ggctgccag ccagctgggt 2261  
ctcccgggac accagcagat ccacaccctg ggcacctcgg tgtttggtct tttttttccc 2321  
ctgtgtgaaa gaagaaacgg caagaccctt tctcaagctg gctcactcag acacattggg 2381  
acaaaccctg gacagccatg ccagagagag gcctttgacc ggccccagag ctaaaagcac 2441  
cagagaaaat caaatgcttc ctactcagcg tgaccaact tttctagtgt gccacggccc 2501  
caccacctcc tgcagtaccc acaccatcac cactgctttc tctccaaca gtgatctgta 2561  
ttcttagttt cattattttc ttttgattga tatgacacta tataaaattt tcatttgaga 2621  
atctctcaat tgtatctagt taaatagcac agtttggaag cttgtctgag actgacttta 2681  
tcaataatct aaccgacaaa gatcatatcc atgtgtatgt ggtagacat tttatttca 2741  
ttgactaacc caggacagtt tcagtgatgc aaattgtgtg cctctgggtt cagctgaaac 2801  
agtcctggac tttcaaaaac cttgaataag tctccacag ttgtataaat tggacaattt 2861  
aggaatttta aacttttagat gatcatttgg ttccattttt atttcatttt tatttttgtt 2921  
aatgcaaaca ggacttaaat gaactttgat ctctgtttta aagattatta aaaaacattg 2981  
tgtatctata catatggctc ttgaggactt agctttcact acactacagg atatgatctc 3041  
catgtagtcc atataaacct gcagagtgat tttccagagt gctcgatact gttaattaca 3101  
tctccattag ggctgaaaag aatgacctac gtttctgtat acagctgtgt tgcttttgat 3161  
gttgtgttac tgtacacaga agtgtgtgca ctgaggctct gcgtgtggtc cgtatggaaa 3221  
acctggtagc cctgcgagtt aagtactgct tccattcatt gtttacgctg gaatttttct 3281  
cccatggaa tgtaagtaaa acttaagtgt ttgtcatcaa taaatggtaa tactaaaaaa 3341  
aaaaaaa 3348

<210> 8

<211> 496

<212> PRT

<213> Homo sapiens

<400> 8

Met	Lys	Leu	Gly	Lys	Lys	Pro	Met	Tyr	Lys	Pro	Val	Asp	Pro	Tyr	Ser
1				5					10					15	

Arg	Met	Gln	Ser	Thr	Tyr	Asn	Tyr	Asn	Met	Arg	Gly	Gly	Ala	Tyr	Pro
			20					25					30		

Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln Val  
 35 40 45

Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr Arg  
 50 55 60

Gln Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu Gln  
 65 70 75 80

Asn Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser Glu  
 85 90 95

Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile Ala  
 100 105 110

Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser Gly  
 115 120 125

Pro Pro His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu Phe  
 130 135 140

Val Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn Ala  
 145 150 155 160

Ala Ile Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro Ala  
 165 170 175

Val Glu Arg Val Lys Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile Val  
 180 185 190

Lys Pro Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile Ser  
 195 200 205

Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu Tyr  
 210 215 220

Thr Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe Val Met  
 225 230 235 240

Gln Val Lys Val Gly Asn His Thr Ala Glu Gly Thr Gly Thr Asn Lys  
 245 250 255

Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu Gly  
 260 265 270

Phe Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser Glu  
 275 280 285

Glu Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr Phe  
 290 295 300

Phe Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu Asp  
 305 310 315 320

Glu	Phe	Arg	Met	Pro	Tyr	Leu	Ser	His	Gln	Gln	Leu	Pro	Ala	Gly	Ile
				325					330					335	
Leu	Pro	Met	Val	Pro	Glu	Val	Ala	Gln	Ala	Val	Gly	Val	Ser	Gln	Gly
			340					345					350		
His	His	Thr	Lys	Asp	Phe	Thr	Arg	Ala	Ala	Pro	Asn	Pro	Ala	Lys	Ala
		355					360					365			
Thr	Val	Thr	Ala	Met	Ile	Ala	Arg	Glu	Leu	Leu	Tyr	Gly	Gly	Thr	Ser
	370					375					380				
Pro	Thr	Ala	Glu	Thr	Ile	Leu	Lys	Asn	Asn	Ile	Ser	Ser	Gly	His	Val
385					390					395					400
Pro	His	Gly	Pro	Leu	Thr	Arg	Pro	Ser	Glu	Gln	Leu	Asp	Tyr	Leu	Ser
				405					410					415	
Arg	Val	Gln	Gly	Phe	Gln	Val	Glu	Tyr	Lys	Asp	Phe	Pro	Lys	Asn	Asn
			420					425					430		
Lys	Asn	Glu	Phe	Val	Ser	Leu	Ile	Asn	Cys	Ser	Ser	Gln	Pro	Pro	Leu
		435					440					445			
Ile	Ser	His	Gly	Ile	Gly	Lys	Asp	Val	Glu	Ser	Cys	His	Asp	Met	Ala
	450					455					460				
Ala	Leu	Asn	Ile	Leu	Lys	Leu	Leu	Ser	Glu	Leu	Asp	Gln	Gln	Ser	Thr
465					470					475					480
Glu	Met	Pro	Arg	Thr	Gly	Asn	Gly	Pro	Met	Ser	Val	Cys	Gly	Arg	Cys
				485					490					495	

<210> 9  
 <211> 2857  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (3)..(1784)

<220>  
 <221> CDS  
 <222> (324)..(1784)

<400> 9																
cg	ggc	gcg	gcc	cct	ccc	ccg	tca	ctt	cct	gcc	agg	ctg	cgg	gcc	ccg	47
	Gly	Ala	Ala	Pro	Pro	Pro	Ser	Leu	Pro	Ala	Arg	Leu	Arg	Ala	Pro	
	1					5				10				15		
agc cgc tct tca gcg ttt gcg ctg gct gtc gtc gcg tct gtg tgc gct															95	



Ser	Arg	Ser	Ser	Ala	Phe	Ala	Leu	Ala	Val	Val	Ala	Ser	Val	Cys	Ala	
				20					25					30		
ccc	cct	tct	tct	gag	ccc	cgg	cct	ggc	ggc	gcc	cgc	ctt	cgc	ctc	cgc	143
Pro	Pro	Ser	Ser	Glu	Pro	Arg	Pro	Gly	Gly	Ala	Arg	Leu	Arg	Leu	Arg	
			35					40					45			
cac	tcc	gcc	tct	tcc	ctc	ctc	tgg	tcg	gcc	cct	ttt	tcc	tcg	ccg	tct	191
His	Ser	Ala	Ser	Ser	Leu	Leu	Trp	Ser	Ala	Pro	Phe	Ser	Ser	Pro	Ser	
		50					55					60				
tca	ctt	gct	tct	tca	cct	cct	cgc	cgc	cgc	cca	aga	ccg	ccg	gcc	ccg	239
Ser	Leu	Ala	Ser	Ser	Pro	Pro	Arg	Arg	Arg	Pro	Arg	Pro	Pro	Ala	Pro	
	65					70				75						
gga	cga	gct	ctg	ggg	aag	cag	cca	gaa	agt	ata	gct	tct	acc	att	gag	287
Gly	Arg	Ala	Leu	Gly	Lys	Gln	Pro	Glu	Ser	Ile	Ala	Ser	Thr	Ile	Glu	
80					85					90					95	
ctc	aat	gca	ctg	tgt	gtg	aaa	ctg	gaa	aga	aaa	cca	atg	tat	aag	ccc	335
Leu	Asn	Ala	Leu	Cys	Val	Lys	Leu	Glu	Arg	Lys	Pro	Met	Tyr	Lys	Pro	
				100					105					110		
gtg	gac	cct	cac	tct	cgg	atg	cag	tcc	acc	tac	agc	tat	ggc	atg	cgt	383
Val	Asp	Pro	His	Ser	Arg	Met	Gln	Ser	Thr	Tyr	Ser	Tyr	Gly	Met	Arg	
			115					120					125			
gga	ggt	gcc	tat	ccc	ccc	aga	tac	ttt	tac	cca	ttt	cca	gtc	cca	cct	431
Gly	Gly	Ala	Tyr	Pro	Pro	Arg	Tyr	Phe	Tyr	Pro	Phe	Pro	Val	Pro	Pro	
		130					135					140				
tta	ctc	tac	caa	gtt	gag	ctc	tcc	gtg	ggc	gga	cag	cag	ttt	aat	ggg	479
Leu	Leu	Tyr	Gln	Val	Glu	Leu	Ser	Val	Gly	Gly	Gln	Gln	Phe	Asn	Gly	
	145					150					155					
aaa	gga	aag	atg	aga	cca	ccc	gtg	aaa	cac	gat	gcc	cct	gcc	cgt	gcg	527
Lys	Gly	Lys	Met	Arg	Pro	Pro	Val	Lys	His	Asp	Ala	Pro	Ala	Arg	Ala	
160					165					170					175	
ctg	agg	act	ctg	cag	agt	gaa	ccc	ctg	cca	gaa	agg	ttg	gag	gta	aat	575
Leu	Arg	Thr	Leu	Gln	Ser	Glu	Pro	Leu	Pro	Glu	Arg	Leu	Glu	Val	Asn	
				180					185					190		
gga	aga	gaa	gca	gag	gaa	gaa	aac	ctc	aat	aaa	tcg	gaa	ata	agc	caa	623
Gly	Arg	Glu	Ala	Glu	Glu	Glu	Asn	Leu	Asn	Lys	Ser	Glu	Ile	Ser	Gln	
			195					200					205			
gtg	ttt	gaa	att	gcg	ctg	aag	cgg	aat	ttg	cct	gtg	aat	ttt	gag	gtg	671
Val	Phe	Glu	Ile	Ala	Leu	Lys	Arg	Asn	Leu	Pro	Val	Asn	Phe	Glu	Val	
		210					215					220				
gcc	cgg	gag	agt	ggc	cca	cca	cac	atg	aag	aac	ttt	gtg	acc	agg	gtt	719
Ala	Arg	Glu	Ser	Gly	Pro	Pro	His	Met	Lys	Asn	Phe	Val	Thr	Arg	Val	
	225					230					235					

tca gtt ggg gaa ttt gta ggg gaa gga gaa ggg aaa agc aag aag atc	767
Ser Val Gly Glu Phe Val Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile	
240 245 250 255	
tcc aag aag aat gcg gcc agg gct gtt ctg gag cag ctt agg agg ctg	815
Ser Lys Lys Asn Ala Ala Arg Ala Val Leu Glu Gln Leu Arg Arg Leu	
260 265 270	
cca ccc ctc cct gct gtg gag cga gtg aag ccc aga atc aag aag aaa	863
Pro Pro Leu Pro Ala Val Glu Arg Val Lys Pro Arg Ile Lys Lys Lys	
275 280 285	
agt cag ccc acc tgc aag aca gcc ccg gat tat ggc caa ggg atg aat	911
Ser Gln Pro Thr Cys Lys Thr Ala Pro Asp Tyr Gly Gln Gly Met Asn	
290 295 300	
cct att agt aga ctt gca cag atc cag cag gca aaa aag gag aag gag	959
Pro Ile Ser Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu	
305 310 315	
cca gag tac atg ctc ctt aca gaa cga ggt ctt cca cgt cgc agg gag	1007
Pro Glu Tyr Met Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu	
320 325 330 335	
ttt gtg atg cag gta aag gtt ggg cat cac act gca gaa gga gtg ggt	1055
Phe Val Met Gln Val Lys Val Gly His His Thr Ala Glu Gly Val Gly	
340 345 350	
acc aat aag aag gtg gcc aag cgt aat gct gct gag aac atg ctg gag	1103
Thr Asn Lys Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu	
355 360 365	
atc ctg ggg ttc aaa gtt ccc cag gcg cag cct gcc aag cca gca ctc	1151
Ile Leu Gly Phe Lys Val Pro Gln Ala Gln Pro Ala Lys Pro Ala Leu	
370 375 380	
aaa tca gaa gag aag act cca gta aag aaa cca gga gac gga agg aaa	1199
Lys Ser Glu Glu Lys Thr Pro Val Lys Lys Pro Gly Asp Gly Arg Lys	
385 390 395	
gta acg ttt ttt gaa cct agc cct ggg gat gaa aat gga act agt aac	1247
Val Thr Phe Phe Glu Pro Ser Pro Gly Asp Glu Asn Gly Thr Ser Asn	
400 405 410 415	
aag gac gag gag ttc agg atg cct tat ctt agc cat cag cag ctg cca	1295
Lys Asp Glu Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro	
420 425 430	
gct gga att ctc ccc atg gtg ccg gaa gtt gcc cag gct gtc ggg gtt	1343
Ala Gly Ile Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val	
435 440 445	
agt caa gga cac cac acc aaa gat ttc acc agg gca gct cca aat cct	1391
Ser Gln Gly His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro	

450	455	460	
gcc aag gca acg gta act gcc atg ata gcc cga gag ttg ttg tac ggg			1439
Ala Lys Ala Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly			
465	470	475	
ggc acc tcg ccc aca gcc gag acc att tta aag agt aac atc tct tca			1487
Gly Thr Ser Pro Thr Ala Glu Thr Ile Leu Lys Ser Asn Ile Ser Ser			
480	485	490	495
ggc cac gta ccc cat gga cct cgc act aga ccc tct gag caa ctg tac			1535
Gly His Val Pro His Gly Pro Arg Thr Arg Pro Ser Glu Gln Leu Tyr			
	500	505	510
tac ctt tcc aga gcc cag gga ttc cag gtt gaa tac aaa gat ttt ccc			1583
Tyr Leu Ser Arg Ala Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro			
	515	520	525
aag aac aac aag aac gag tgt gta tct ctc atc aac tgc tcc tca cag			1631
Lys Asn Asn Lys Asn Glu Cys Val Ser Leu Ile Asn Cys Ser Ser Gln			
	530	535	540
ccg cct ctc gtc agt cat ggc atc ggc aag gat gtg gag tcc tgt cat			1679
Pro Pro Leu Val Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His			
	545	550	555
gat atg gct gca ctg aac att tta aag ctg ctg tct gag ttg gac caa			1727
Asp Met Ala Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln			
560	565	570	575
cag agc aca gag atg cca aga aca gga aat gga cca gtt tca gcg tgc			1775
Gln Ser Thr Glu Met Pro Arg Thr Gly Asn Gly Pro Val Ser Ala Cys			
	580	585	590
ggg agg tgc tgaacctttt ctggccacaa accattataa aacccaacat			1824
Gly Arg Cys			
atatactgaa aatactgaga actgctttga aaatttgga tctctgataa ctccagtggg			1884
ccaagacatg gtggataaaa atgtggcaaa gacgacaaga aacttcaggt ggtagccctg			1944
gttgtgctgg cggctagtga tgatgctgtg ctctgccatc catccagaca gaaaccagcc			2004
ccaacgcctc cagttctgtt ttgcatcgt gacaaagaga gcacagccaa ttctcatgct			2064
ggctttcttca gatactttga aaaacccgga cagccacacc agagaggcct tatagcggcc			2124
ccggagctaa acggaccaga gaaaaggcca gtgcttccta ctgcacatga ctgactcagc			2184
tccgccacac gtagcaccac tgtaaccact gctttctctt cagtttcatt ttttccctt			2244
gattgataca acactataat tttcatttca gttccttagt cgtgtctact tacctagcag			2304
tttagaaaact gtcagtcatg taactggcaa ggatcacagc ccggttggtt ggcattctgt			2364

gcctctggct tggctgaaca gttctggaat taccaccaga atccttgact ccctgcccct 2424  
 tgtataaatt ggacagctta ggacttttaa acttttagatc aaaagatatg gtccttttta 2484  
 actttatttt taaggagcag actttaaaat gagccctgac ctttaccat tataacagaa 2544  
 tttgtcaaaa ggagtgttct ttgaggaggt agcttttttt taccacacta caggacatta 2604  
 cctgtaggcc cagaagacta caggctggtg tccctagagg gcccaatata gtcaattcca 2664  
 acctctaagt cggggaaagg tgacaggttt cctggtgctg gtgtgcacag gggcaggcag 2724  
 gtcagctggc ctggggaaga gcattgtggc tcctagtgc gccctgcttc cactcttggg 2784  
 ttagctggaa ccttcccact catggaatat aagtaaactc actttctttg tcaccaataa 2844  
 atggtataac taa 2857

<210> 10  
 <211> 594  
 <212> PRT  
 <213> Mus musculus

<400> 10  
 Gly Ala Ala Pro Pro Pro Ser Leu Pro Ala Arg Leu Arg Ala Pro Ser  
 1 5 10 15  
 Arg Ser Ser Ala Phe Ala Leu Ala Val Val Ala Ser Val Cys Ala Pro  
 20 25 30  
 Pro Ser Ser Glu Pro Arg Pro Gly Gly Ala Arg Leu Arg Leu Arg His  
 35 40 45  
 Ser Ala Ser Ser Leu Leu Trp Ser Ala Pro Phe Ser Ser Pro Ser Ser  
 50 55 60  
 Leu Ala Ser Ser Pro Pro Arg Arg Arg Pro Arg Pro Pro Ala Pro Gly  
 65 70 75 80  
 Arg Ala Leu Gly Lys Gln Pro Glu Ser Ile Ala Ser Thr Ile Glu Leu  
 85 90 95  
 Asn Ala Leu Cys Val Lys Leu Glu Arg Lys Pro Met Tyr Lys Pro Val  
 100 105 110  
 Asp Pro His Ser Arg Met Gln Ser Thr Tyr Ser Tyr Gly Met Arg Gly  
 115 120 125  
 Gly Ala Tyr Pro Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu  
 130 135 140  
 Leu Tyr Gln Val Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys  
 145 150 155 160  
 Gly Lys Met Arg Pro Pro Val Lys His Asp Ala Pro Ala Arg Ala Leu  
 165 170 175  
 Arg Thr Leu Gln Ser Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly  
 180 185 190  
 Arg Glu Ala Glu Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val  
 195 200 205  
 Phe Glu Ile Ala Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala  
 210 215 220  
 Arg Glu Ser Gly Pro Pro His Met Lys Asn Phe Val Thr Arg Val Ser

225					230					235				240
Val	Gly	Glu	Phe	Val	Gly	Glu	Gly	Glu	Gly	Lys	Ser	Lys	Lys	Ile
				245					250					255
Lys	Lys	Asn	Ala	Ala	Arg	Ala	Val	Leu	Glu	Gln	Leu	Arg	Arg	Leu
			260					265					270	Pro
Pro	Leu	Pro	Ala	Val	Glu	Arg	Val	Lys	Pro	Arg	Ile	Lys	Lys	Lys
		275					280					285		Ser
Gln	Pro	Thr	Cys	Lys	Thr	Ala	Pro	Asp	Tyr	Gly	Gln	Gly	Met	Asn
	290					295					300			Pro
Ile	Ser	Arg	Leu	Ala	Gln	Ile	Gln	Gln	Ala	Lys	Lys	Glu	Lys	Glu
305					310					315				320
Glu	Tyr	Met	Leu	Leu	Thr	Glu	Arg	Gly	Leu	Pro	Arg	Arg	Arg	Glu
			325						330					335
Val	Met	Gln	Val	Lys	Val	Gly	His	His	Thr	Ala	Glu	Gly	Val	Gly
			340					345					350	Thr
Asn	Lys	Lys	Val	Ala	Lys	Arg	Asn	Ala	Ala	Glu	Asn	Met	Leu	Glu
	355						360					365		Ile
Leu	Gly	Phe	Lys	Val	Pro	Gln	Ala	Gln	Pro	Ala	Lys	Pro	Ala	Leu
	370					375					380			Lys
Ser	Glu	Glu	Lys	Thr	Pro	Val	Lys	Lys	Pro	Gly	Asp	Gly	Arg	Lys
385					390					395				400
Thr	Phe	Phe	Glu	Pro	Ser	Pro	Gly	Asp	Glu	Asn	Gly	Thr	Ser	Asn
				405					410					415
Asp	Glu	Glu	Phe	Arg	Met	Pro	Tyr	Leu	Ser	His	Gln	Gln	Leu	Pro
			420					425					430	Ala
Gly	Ile	Leu	Pro	Met	Val	Pro	Glu	Val	Ala	Gln	Ala	Val	Gly	Val
	435						440					445		Ser
Gln	Gly	His	His	Thr	Lys	Asp	Phe	Thr	Arg	Ala	Ala	Pro	Asn	Pro
	450					455					460			Ala
Lys	Ala	Thr	Val	Thr	Ala	Met	Ile	Ala	Arg	Glu	Leu	Leu	Tyr	Gly
465					470					475				480
Thr	Ser	Pro	Thr	Ala	Glu	Thr	Ile	Leu	Lys	Ser	Asn	Ile	Ser	Ser
				485					490					495
His	Val	Pro	His	Gly	Pro	Arg	Thr	Arg	Pro	Ser	Glu	Gln	Leu	Tyr
		500					505						510	Tyr
Leu	Ser	Arg	Ala	Gln	Gly	Phe	Gln	Val	Glu	Tyr	Lys	Asp	Phe	Pro
	515					520					525			Lys
Asn	Asn	Lys	Asn	Glu	Cys	Val	Ser	Leu	Ile	Asn	Cys	Ser	Ser	Gln
	530					535				540				Pro
Pro	Leu	Val	Ser	His	Gly	Ile	Gly	Lys	Asp	Val	Glu	Ser	Cys	His
545					550				555					560
Met	Ala	Ala	Leu	Asn	Ile	Leu	Lys	Leu	Leu	Ser	Glu	Leu	Asp	Gln
			565					570					575	Gln
Ser	Thr	Glu	Met	Pro	Arg	Thr	Gly	Asn	Gly	Pro	Val	Ser	Ala	Cys
			580					585					590	Gly
Arg	Cys													

<210> 11  
 <211> 487  
 <212> PRT  
 <213> Mus musculus

<400> 11

Met	Tyr	Lys	Pro	Val	Asp	Pro	His	Ser	Arg	Met	Gln	Ser	Thr	Tyr	Ser	1	5	10	15
Tyr	Gly	Met	Arg	Gly	Gly	Ala	Tyr	Pro	Pro	Arg	Tyr	Phe	Tyr	Pro	Phe	20	25	30	
Pro	Val	Pro	Pro	Leu	Leu	Tyr	Gln	Val	Glu	Leu	Ser	Val	Gly	Gly	Gln	35	40	45	
Gln	Phe	Asn	Gly	Lys	Gly	Lys	Met	Arg	Pro	Pro	Val	Lys	His	Asp	Ala	50	55	60	
Pro	Ala	Arg	Ala	Leu	Arg	Thr	Leu	Gln	Ser	Glu	Pro	Leu	Pro	Glu	Arg	65	70	75	80
Leu	Glu	Val	Asn	Gly	Arg	Glu	Ala	Glu	Glu	Glu	Asn	Leu	Asn	Lys	Ser	85	90	95	
Glu	Ile	Ser	Gln	Val	Phe	Glu	Ile	Ala	Leu	Lys	Arg	Asn	Leu	Pro	Val	100	105	110	
Asn	Phe	Glu	Val	Ala	Arg	Glu	Ser	Gly	Pro	Pro	His	Met	Lys	Asn	Phe	115	120	125	
Val	Thr	Arg	Val	Ser	Val	Gly	Glu	Phe	Val	Gly	Glu	Gly	Glu	Gly	Lys	130	135	140	
Ser	Lys	Lys	Ile	Ser	Lys	Lys	Asn	Ala	Ala	Arg	Ala	Val	Leu	Glu	Gln	145	150	155	160
Leu	Arg	Arg	Leu	Pro	Pro	Leu	Pro	Ala	Val	Glu	Arg	Val	Lys	Pro	Arg	165	170	175	
Ile	Lys	Lys	Lys	Ser	Gln	Pro	Thr	Cys	Lys	Thr	Ala	Pro	Asp	Tyr	Gly	180	185	190	
Gln	Gly	Met	Asn	Pro	Ile	Ser	Arg	Leu	Ala	Gln	Ile	Gln	Gln	Ala	Lys	195	200	205	
Lys	Glu	Lys	Glu	Pro	Glu	Tyr	Met	Leu	Leu	Thr	Glu	Arg	Gly	Leu	Pro	210	215	220	
Arg	Arg	Arg	Glu	Phe	Val	Met	Gln	Val	Lys	Val	Gly	His	His	Thr	Ala	225	230	235	240
Glu	Gly	Val	Gly	Thr	Asn	Lys	Lys	Val	Ala	Lys	Arg	Asn	Ala	Ala	Glu	245	250	255	
Asn	Met	Leu	Glu	Ile	Leu	Gly	Phe	Lys	Val	Pro	Gln	Ala	Gln	Pro	Ala	260	265	270	
Lys	Pro	Ala	Leu	Lys	Ser	Glu	Glu	Lys	Thr	Pro	Val	Lys	Lys	Pro	Gly	275	280	285	
Asp	Gly	Arg	Lys	Val	Thr	Phe	Phe	Glu	Pro	Ser	Pro	Gly	Asp	Glu	Asn	290	295	300	
Gly	Thr	Ser	Asn	Lys	Asp	Glu	Glu	Phe	Arg	Met	Pro	Tyr	Leu	Ser	His	305	310	315	320
Gln	Gln	Leu	Pro	Ala	Gly	Ile	Leu	Pro	Met	Val	Pro	Glu	Val	Ala	Gln	325	330	335	
Ala	Val	Gly	Val	Ser	Gln	Gly	His	His	Thr	Lys	Asp	Phe	Thr	Arg	Ala	340	345	350	
Ala	Pro	Asn	Pro	Ala	Lys	Ala	Thr	Val	Thr	Ala	Met	Ile	Ala	Arg	Glu	355	360	365	
Leu	Leu	Tyr	Gly	Gly	Thr	Ser	Pro	Thr	Ala	Glu	Thr	Ile	Leu	Lys	Ser	370	375	380	
Asn	Ile	Ser	Ser	Gly	His	Val	Pro	His	Gly	Pro	Arg	Thr	Arg	Pro	Ser	385	390	395	400
Glu	Gln	Leu	Tyr	Tyr	Leu	Ser	Arg	Ala	Gln	Gly	Phe	Gln	Val	Glu	Tyr	405	410	415	
Lys	Asp	Phe	Pro	Lys	Asn	Asn	Lys	Asn	Glu	Cys	Val	Ser	Leu	Ile	Asn	420	425	430	

Cys Ser Ser Gln Pro Pro Leu Val Ser His Gly Ile Gly Lys Asp Val  
           435                          440                          445  
 Glu Ser Cys His Asp Met Ala Ala Leu Asn Ile Leu Lys Leu Leu Ser  
           450                          455                          460  
 Glu Leu Asp Gln Gln Ser Thr Glu Met Pro Arg Thr Gly Asn Gly Pro  
 465                          470                          475                          480  
 Val Ser Ala Cys Gly Arg Cys  
                           485

<210> 12  
 <211> 16  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: unknown

<400> 12  
 Ala Gly Cys Thr Thr Ala Ala Thr Thr Ala Gly Cys Thr Gly Ala Cys  
   1                          5                          10                          15

<210> 13  
 <211> 16  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: unknown

<400> 13  
 Ala Gly Cys Thr Gly Thr Cys Ala Gly Cys Thr Ala Ala Thr Thr Ala  
   1                          5                          10                          15

<210> 14  
 <211> 31  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: unknown

<400> 14  
 Cys Cys Thr Gly Gly Ala Thr Cys Cys Gly Ala Ala Ala Gly Thr Ala  
   1                          5                          10                          15

Thr Ala Gly Cys Thr Thr Cys Thr Ala Cys Cys Ala Thr Thr Gly  
                           20                          25                          30

<210> 15

<211> 31  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: unknown

<400> 15  
Cys Cys Thr Gly Gly Ala Thr Cys Cys Gly Ala Ala Ala Gly Thr Ala  
1 5 10 15  
Thr Ala Gly Cys Thr Thr Cys Thr Ala Cys Cys Ala Thr Thr Gly  
20 25 30

<210> 16  
<211> 36  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: unknown

<400> 16  
Thr Ala Cys Ala Thr Ala Ala Gly Cys Thr Thr Cys Thr Ala Gly Ala  
1 5 10 15  
Thr Gly Gly Cys Cys Ala Gly Ala Ala Ala Gly Gly Thr Thr Cys  
20 25 30  
Ala Gly Cys Ala  
35

<210> 17  
<211> 27  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: unknown

<400> 17  
Gly Gly Ala Thr Gly Ala Ala Thr Cys Cys Thr Ala Thr Thr Ala Gly  
1 5 10 15  
Thr Ala Gly Ala Cys Thr Thr Gly Cys Ala Cys  
20 25

<210> 18  
<211> 29  
<212> PRT  
<213> Unknown Organism



<220>

<223> Description of Unknown Organism: unknown

<400> 18

Gly Cys Thr Cys Thr Ala Gly Ala Thr Thr Cys Ala Ala Ala Gly Thr  
1 5 10 15

Thr Cys Cys Cys Cys Ala Gly Gly Cys Gly Cys Ala Gly  
20 25

<210> 19

<211> 29

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: unknown

<400> 19

Thr Thr Thr Ala Ala Gly Cys Thr Thr Cys Thr Cys Ala Gly Ala Gly  
1 5 10 15

Gly Gly Thr Cys Thr Ala Gly Thr Gly Cys Gly Ala Gly  
20 25

<210> 20

<211> 22

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: unknown

<400> 20

Cys Ala Ala Thr Gly Thr Ala Thr Ala Ala Gly Cys Cys Cys Gly Thr  
1 5 10 15

Gly Gly Ala Cys Cys Cys  
20

<210> 21

<211> 36

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: unknown

<400> 21

Ala Ala Ala Ala Ala Gly Cys Thr Thr Gly Thr Gly Cys Ala Ala Gly  
1 5 10 15

Thr Cys Thr Ala Cys Thr Ala Ala Thr Ala Gly Gly Ala Thr Thr Cys  
20 25 30

Ala Thr Cys Cys  
35

<210> 22  
<211> 18  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: unknown

<400> 22  
Ala Thr Ala Gly Cys Cys Cys Gly Ala Gly Ala Gly Thr Thr Gly Thr  
1 5 10 15

Thr Gly

<210> 23  
<211> 36  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: unknown

<400> 23  
Thr Ala Cys Ala Thr Ala Ala Gly Cys Thr Thr Cys Thr Ala Gly Ala  
1 5 10 15

Thr Gly Gly Cys Cys Ala Gly Ala Ala Ala Gly Gly Thr Thr Cys  
20 25 30

Ala Gly Cys Ala  
35

<210> 24  
<211> 29  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: unknown

<400> 24  
Thr Ala Cys Ala Thr Gly Thr Cys Gly Ala Cys Thr Thr Cys Cys Thr  
1 5 10 15

Gly Cys Cys Arg Gly Gly Cys Thr Gly Cys Gly Gly Gly  
20 25

<210> 25  
<211> 44  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: unknown

<400> 25  
Thr Ala Cys Ala Ala Thr Cys Thr Ala Gly Ala Thr Thr Ala Thr Cys  
1 5 10 15  
Ala Gly Cys Gly Gly Cys Cys Gly Cys Ala Cys Cys Thr Cys Cys Cys  
20 25 30  
Ala Cys Ala Cys Ala Cys Ala Gly Ala Cys Ala Thr  
35 40

<210> 26  
<211> 41  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: unknown

<400> 26  
Thr Ala Cys Ala Thr Ala Ala Gly Cys Thr Thr Ala Ala Gly Cys Cys  
1 5 10 15  
Ala Cys Cys Ala Thr Gly Gly Thr Cys Ala Ala Ala Gly Thr Thr Cys  
20 25 30  
Cys Cys Cys Ala Gly Gly Cys Gly Cys  
35 40

<210> 27  
<211> 40  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: unknown

<400> 27  
Thr Ala Cys Ala Ala Thr Cys Thr Ala Gly Ala Gly Cys Gly Gly Cys  
1 5 10 15

Cys Gly Cys Gly Cys Thr Cys Ala Gly Ala Gly Gly Gly Thr Cys Thr  
20 25 30

Ala Gly Thr Gly Cys Gly Ala Gly  
35 40